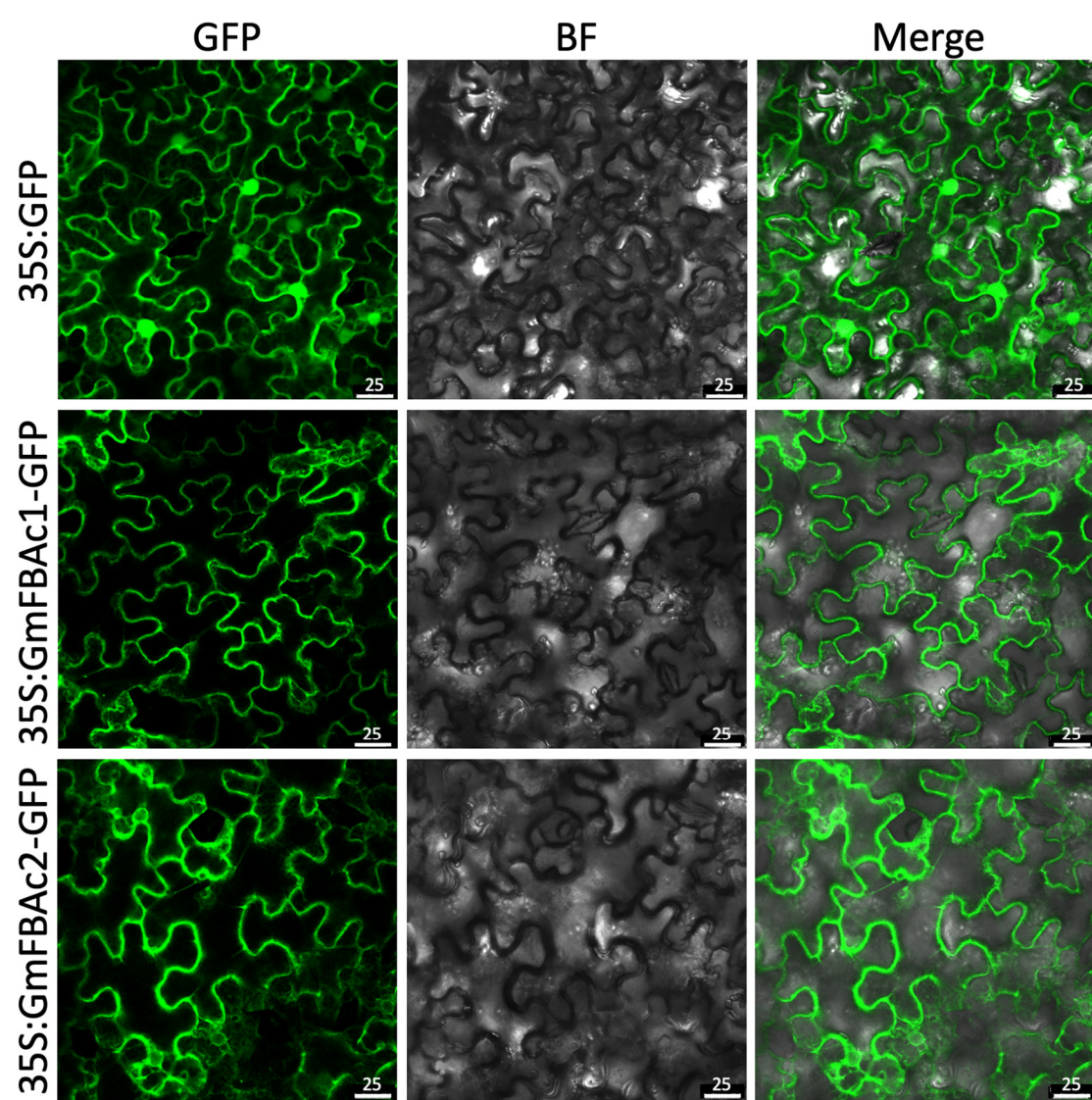


**Figure S1.** Gene structure of *GmFBA* family. Blue strip represents UTR, and yellow strip represent coding sequencing.

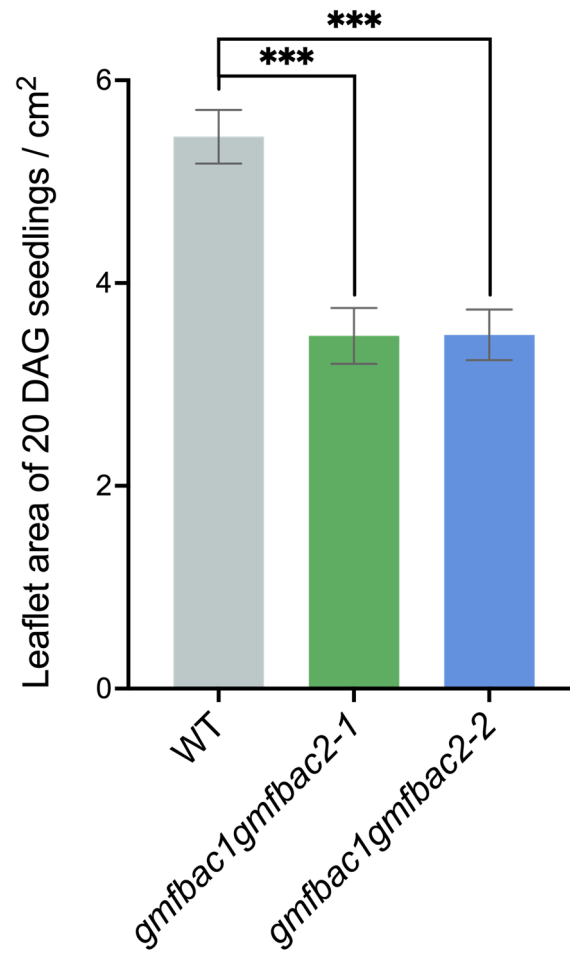


**Figure S2.** Subcellular localization of GmFBAc1 and GmFBAc2. The left panel shows the image of GFP channel, the middle panel shows image of bright field and the right panel shows the merge image of GFP channel and bright field. Bar = 25  $\mu$ m.

5 DAG

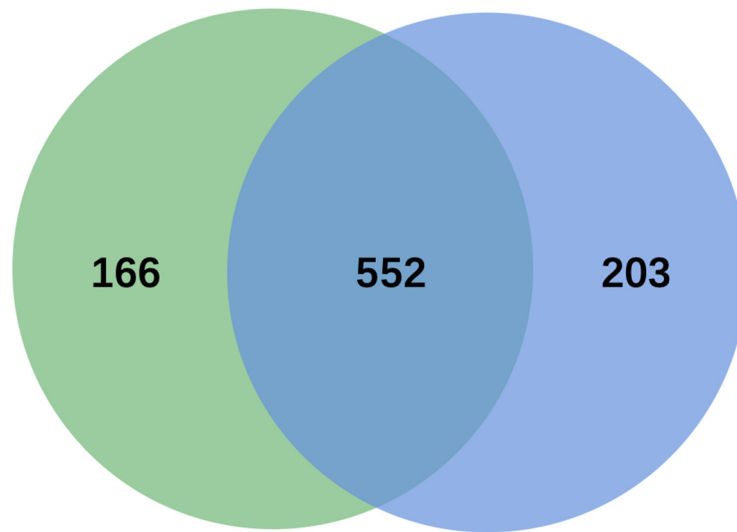


**Figure S3.** Phenotype of 5 DAG soybean seedlings of wild type and *gmfbac1gmfbac2* mutants. Bar = 2 cm.



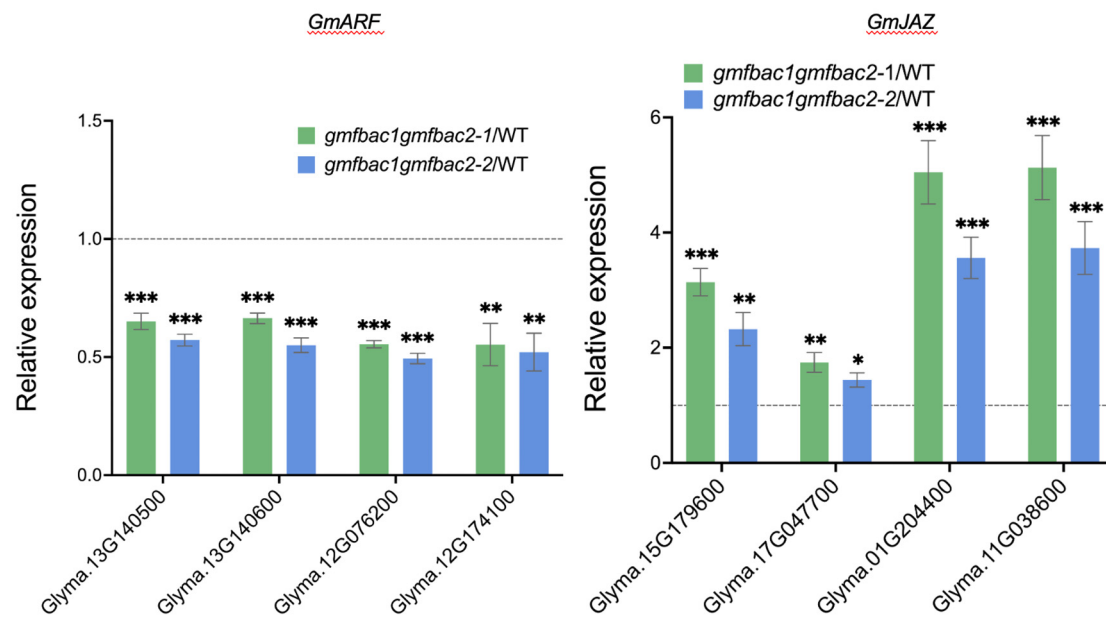
**Figure S4.** Leaflet area of 20 DAG wild type and *gmfbac1gmfbac2* seedlings. All values are presented as the mean  $\pm$  SEM. t-test was performed between WT and *gmfbac1gmfbac2* mutants. \*\*\*  $p < 0.001$ .

***gmfbac1gmfbac2-1* vs WT**



***gmfbac1gmfbac2-2* vs WT**

**Figure S5.** Venn plot of DEGs in two lines of *gmfbac1gmfbac2* vs wild type, respectively. RNAseq analysis identified 718 DEGs between *gmfbac1gmfbac2-1* and wild type, and 755 DEGs between *gmfbac1gmfbac2-2* and wild type.



**Figure S6.** Relative expression of *GmARF* and *GmJAZ* in *gmfbac1gmfbac2* leaves was verified by RT-qPCR.  $2^{-\Delta\Delta C_t}$  was used for calculating the relative expression. \*  $p < 0.05$ , \*\*  $p < 0.01$ , \*\*\*  $p < 0.001$ .